

CRF Errors Corrected by the STIC Systems Branch

O/PK 0570  
0125

Serial Number: 10/026,767

CRF Processing Date: 1/19/2002

Edited by: [Signature]

Verified by: [Signature] (STIC staff)

**ENTERED**

#2

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

## RAW SEQUENCE LISTING

DATE: 01/19/2002

PATENT APPLICATION: US/10/026,767

TIME: 14:40:57

Input Set : A:\PTO.txt

Output Set: N:\CRF3\01182002\J026767.raw

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1 <110> APPLICANT: Hitachi, LTD.
2     RIKEN
3     Japan International Research Center for Agricultural Science
4     Bio-oriented Technology Research Advancement Institute (BRAIN)
6 <120> TITLE OF INVENTION: Transgenic rice plant and its family with environmental
7     stress resistant by proline accumulation of high level and its
8     production.
10 <130> FILE REFERENCE: NT01P0353
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/026,767
C--> 12 <141> CURRENT FILING DATE: 2001-12-27
12 <160> NUMBER OF SEQ ID NOS: 3
14 <210> SEQ ID NO: 1
16 <211> LENGTH: 2549
18 <212> TYPE: DNA
20 <213> ORGANISM: Oryza sativa L.
22 <220> FEATURE:
24 <221> NAME/KEY: CDS
26 <222> LOCATION: 99..2249
28 <300> PUBLICATION INFORMATION:
30 <301> AUTHORS: Yumiko Igarashi, Yoshu Yoshiba, Yukika Sanada, Kazuko
31     Yamaguchi-Shinozaki, Keishiro Wada, Kazuo Shinozaki
33 <302> TITLE: Characterization of the gene for 1-pyrroline-5-carboxylate
34     synthetase and correlation between the expression of the gene and
35     salt tolerance in Oryza sativa L.
37 <303> JOURNAL: Plant Molecular biology
39 <304> VOLUME: 33
41 <306> PAGES: 857-865
43 <307> DATE: 1996-12-03
45 <308> DATABASE ACCESSION NO: D49714
47 <309> DATABASE ENTRY DATE: 1995-03-16
49 <400> SEQUENCE: 1
51 gcggtctgcgg cggcaaggcg gcgagacgtg ggagagggat ttacaggtag agggagaggg 60
55 tggaggagga gaggctgagg ctaggaagcg gtttcgcc atg gcg agc gtc gac ccg 116
57                                     Met Ala Ser Val Asp Pro
59                                     1           5
63 tcc cgg agc ttc gtg agg gac gtg aag cgc gtc atc atc aag gtg ggc 164
65 Ser Arg Ser Phe Val Arg Asp Val Lys Arg Val Ile Ile Lys Val Gly
67         10           15           20
71 act gca gtt gtc tcc aga caa gat gga aga ttg gct ttg ggc agg gtt 212
73 Thr Ala Val Val Ser Arg Gln Asp Gly Arg Leu Ala Leu Gly Arg Val
75         25           30           35
79 gga gct ctg tgc gag cag gtt aag gaa ctg aac tct tta gga tac gaa 260
81 Gly Ala Leu Cys Glu Gln Val Lys Glu Leu Asn Ser Leu Gly Tyr Glu

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89	Val Ile Leu Val Thr Ser Gly Ala Val Gly Val Gly Arg Gln Arg Leu			
91	55 60 65 70			
95	agg tac cgg aag ctt gtc aat agc agc ttt gct gat ctg caa aag cca	356		
97	Arg Tyr Arg Lys Leu Val Asn Ser Ser Phe Ala Asp Leu Gln Lys Pro			
99	75 80 85			
103	cag atg gag tta gat gga aag gct tgt gcc gct gtt ggt cag agt gga	404		
105	Gln Met Glu Leu Asp Gly Lys Ala Cys Ala Ala Val Gly Gln Ser Gly			
107	90 95 100			
111	ctg atg gct ctt tac gat atg ttg ttt aac caa ctg gat gtc tcg tca	452		
113	Leu Met Ala Leu Tyr Asp Met Leu Phe Asn Gln Leu Asp Val Ser Ser			
115	105 110 115			
119	tct caa ctt ctt gtc acc gac agt gat ttt gag aac cca aag ttc cgg	500		
121	Ser Gln Leu Leu Val Thr Asp Ser Asp Phe Glu Asn Pro Lys Phe Arg			
123	120 125 130			
127	gag caa ctc act gaa act gtt gag tca tta tta gat ctt aaa gtt ata	548		
129	Glu Gln Leu Thr Glu Thr Val Glu Ser Leu Leu Asp Leu Lys Val Ile			
131	135 140 145 150			
135	cca ata ttt aat gaa aat gat gcc atc agc act aga aag gct cca tat	596		
137	Pro Ile Phe Asn Glu Asn Asp Ala Ile Ser Thr Arg Lys Ala Pro Tyr			
139	155 160 165			
143	gag gat tca tct ggt ata ttc tgg gat aat gac agt tta gca gga ctg	644		
145	Glu Asp Ser Ser Gly Ile Phe Trp Asp Asn Asp Ser Leu Ala Gly Leu			
147	170 175 180			
151	ttg gca ctg gaa ctg aaa gct gat ctc ctt att ctg ctc agt gat gtg	692		
153	Leu Ala Leu Glu Leu Lys Ala Asp Leu Leu Ile Leu Leu Ser Asp Val			
155	185 190 195			
159	gat ggg ttg tat agt ggt cca cca agt gaa cca tca tca aaa atc ata	740		
161	Asp Gly Leu Tyr Ser Gly Pro Pro Ser Glu Pro Ser Ser Lys Ile Ile			
163	200 205 210			
167	cac act tat att aaa gaa aag cat cag caa gaa atc act ttt gga gac	788		
169	His Thr Tyr Ile Lys Glu Lys His Gln Gln Glu Ile Thr Phe Gly Asp			
171	215 220 225 230			
175	aaa tct cgt gta ggt aga gga ggc atg aca gca aaa gtg aag gct gct	836		
177	Lys Ser Arg Val Gly Arg Gly Gly Met Thr Ala Lys Val Lys Ala Ala			
179	235 240 245			
183	gtc ttg gct tca aat agc ggc aca cct gtg gtt att aca agt ggg ttt	884		
185	Val Leu Ala Ser Asn Ser Gly Thr Pro Val Val Ile Thr Ser Gly Phe			
187	250 255 260			
191	gaa aat cgg agc att ctt aaa gtt ctt cat ggg gaa aaa att ggt act	932		
193	Glu Asn Arg Ser Ile Leu Lys Val Leu His Gly Glu Lys Ile Gly Thr			
195	265 270 275			
199	ctc ttt cac aag aat gcg aat ttg tgg gaa tca tct aag gat gtt agt	980		
201	Leu Phe His Lys Asn Ala Asn Leu Trp Glu Ser Ser Lys Asp Val Ser			
203	280 285 290			
207	act cgt gag atg gct gtt gcc gca aga gat tgt tca agg cat cta cag	1028		
209	Thr Arg Glu Met Ala Val Ala Ala Arg Asp Cys Ser Arg His Leu Gln			
211	295 300 305 310			

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217	Asn	Leu	Ser	Ser	Glu	Glu	Arg	Lys	Lys	Ile	Leu	Leu	Asp	Val	Ala	Asp	
219					315					320					325		
223	gct	ttg	gag	gca	aat	gag	gat	tta	ata	agg	tct	gag	aat	gaa	gct	gat	1124
225	Ala	Leu	Glu	Ala	Asn	Glu	Asp	Leu	Ile	Arg	Ser	Glu	Asn	Glu	Ala	Asp	
227				330					335					340			
231	gta	gct	gcg	gcc	caa	gtt	gct	gga	tat	gag	aag	cct	ttg	gtt	gct	aga	1172
233	Val	Ala	Ala	Ala	Gln	Val	Ala	Gly	Tyr	Glu	Lys	Pro	Leu	Val	Ala	Arg	
235			345					350					355				
239	ttg	act	ata	aaa	cca	gga	aag	ata	gca	agc	ctt	gca	aaa	tct	att	cgt	1220
241	Leu	Thr	Ile	Lys	Pro	Gly	Lys	Ile	Ala	Ser	Leu	Ala	Lys	Ser	Ile	Arg	
243		360				365					370						
247	acc	ctt	gca	aat	atg	gaa	gac	cct	ata	aac	cag	ata	ctt	aaa	aag	aca	1268
249	Thr	Leu	Ala	Asn	Met	Glu	Asp	Pro	Ile	Asn	Gln	Ile	Leu	Lys	Lys	Thr	
251	375					380				385					390		
255	gag	gtt	gct	gat	gat	tta	gtt	ctt	gag	aaa	aca	tct	tgc	cca	tta	ggt	1316
257	Glu	Val	Ala	Asp	Asp	Leu	Val	Leu	Glu	Lys	Thr	Ser	Cys	Pro	Leu	Gly	
259				395					400					405			
263	gtt	ctc	tta	att	gtt	ttt	gag	tcc	cga	cct	gat	gcc	ttg	gtt	cag	att	1364
265	Val	Leu	Leu	Ile	Val	Phe	Glu	Ser	Arg	Pro	Asp	Ala	Leu	Val	Gln	Ile	
267			410					415					420				
271	gca	tct	ttg	gca	att	cga	agt	ggt	aat	ggt	ctt	ctc	cta	aaa	ggt	gga	1412
273	Ala	Ser	Leu	Ala	Ile	Arg	Ser	Gly	Asn	Gly	Leu	Leu	Leu	Lys	Gly	Gly	
275		425				430					435						
279	aaa	gaa	gct	atc	aga	tca	aac	acg	ata	ttg	cat	aag	gtt	ata	act	gat	1460
281	Lys	Glu	Ala	Ile	Arg	Ser	Asn	Thr	Ile	Leu	His	Lys	Val	Ile	Thr	Asp	
283		440				445					450						
287	gct	att	cct	cgt	aat	gtt	ggt	gaa	aaa	ctt	att	ggc	ctt	gtt	aca	act	1508
289	Ala	Ile	Pro	Arg	Asn	Val	Gly	Glu	Lys	Leu	Ile	Gly	Leu	Val	Thr	Thr	
291	455				460				465					470			
295	aga	gat	gag	atc	gca	gat	ttg	cta	aag	ctt	gat	gat	gtc	att	gat	ctt	1556
297	Arg	Asp	Glu	Ile	Ala	Asp	Leu	Leu	Lys	Leu	Asp	Asp	Val	Ile	Asp	Leu	
299			475					480					485				
303	gtc	act	cca	aga	gga	agt	aat	aag	ctt	gtc	tct	caa	atc	aag	gcg	tca	1604
305	Val	Thr	Pro	Arg	Gly	Ser	Asn	Lys	Leu	Val	Ser	Gln	Ile	Lys	Ala	Ser	
307			490					495					500				
311	act	aag	att	cct	gtt	ctt	ggg	cat	gct	gat	ggt	ata	tgc	cac	gta	tat	1652
313	Thr	Lys	Ile	Pro	Val	Leu	Gly	His	Ala	Asp	Gly	Ile	Cys	His	Val	Tyr	
315		505				510					515						
319	att	gac	aaa	tca	gct	gac	atg	gat	atg	gca	aaa	ctt	att	gta	atg	gat	1700
321	Ile	Asp	Lys	Ser	Ala	Asp	Met	Asp	Met	Ala	Lys	Leu	Ile	Val	Met	Asp	
323		520				525					530						
327	gca	aaa	act	gat	tac	cca	gca	gcc	tgc	aat	gca	atg	gag	acc	tta	cta	1748
329	Ala	Lys	Thr	Asp	Tyr	Pro	Ala	Ala	Cys	Asn	Ala	Met	Glu	Thr	Leu	Leu	
331	535				540				545				550				
335	gtt	cat	aag	gat	ctt	atg	aag	agt	cca	ggc	ctt	gac	gac	ata	tta	gta	1796
337	Val	His	Lys	Asp	Leu	Met	Lys	Ser	Pro	Gly	Leu	Asp	Asp	Ile	Leu	Val	
339			555					560					565				
343	gca	cta	aaa	aca	gaa	gga	gtt	aat	att	tat	ggt	gga	cct	att	gcg	cac	1844

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351 aaa gct ctg gga ttt cca aaa gct gtt tca ttt cat cat gag tat agt 1892
353 Lys Ala Leu Gly Phe Pro Lys Ala Val Ser Phe His His Glu Tyr Ser
355          585          590          595
359 tct atg gcc tgc act gtt gag ttt gtt gat gat gtt caa tca gca att 1940
361 Ser Met Ala Cys Thr Val Glu Phe Val Asp Asp Val Gln Ser Ala Ile
363          600          605          610
367 gac cat att cat cgt tat gga agt gct cat aca gat tgt atc gtc act 1988
369 Asp His Ile His Arg Tyr Gly Ser Ala His Thr Asp Cys Ile Val Thr
371 615          620          625          630
375 aca gat gat aag gta gca gag act ttt cta cgc aga gtt gat agt gct 2036
377 Thr Asp Asp Lys Val Ala Glu Thr Phe Leu Arg Arg Val Asp Ser Ala
379          635          640          645
383 gct gta ttt cat aat gca agt acg aga ttc tct gat ggg gct cgt ttt 2084
385 Ala Val Phe His Asn Ala Ser Thr Arg Phe Ser Asp Gly Ala Arg Phe
387          650          655          660
391 gga ttg ggt gct gag gtt ggc ata agc aca ggg cgt atc cat gcc cgt 2132
393 Gly Leu Gly Ala Glu Val Gly Ile Ser Thr Gly Arg Ile His Ala Arg
395          665          670          675
399 gga cca gtg ggt gtt gaa ggt ctc tta act aca cga tgg atc ttg cga 2180
401 Gly Pro Val Gly Val Glu Gly Leu Leu Thr Thr Arg Trp Ile Leu Arg
403          680          685          690
407 gga cgt ggg caa gtg gtg aat ggt gac aag gat gtc gtg tac acc cat 2228
409 Gly Arg Gly Gln Val Val Asn Gly Asp Lys Asp Val Val Tyr Thr His
411 695          700          705          710
415 aag agt ctt cct ttg caa tgaggtcaaa tgctcctttt agcctgttca 2276
417 Lys Ser Leu Pro Leu Gln
419          715
423 ggagtaggtg aatatacctt taagaatgga ttgactactt tattttgtca tcttgtacaa 2336
427 gcatcttatt gcggcattcc gatggattat tgattttggg ggttcccact ttcaaagtgt 2396
431 acaccaaaaa taaattcatc agttctgaga gcaagatttt ggaggttcag cttctccatg 2456
435 taataagtaa attcagttct gagaacttgt gtaccaacgc gctatgttgc ttgtaatgag 2516
439 cgatactaac atctgtgatt gcacatatat taa 2549
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444 <211> LENGTH: 2571
446 <212> TYPE: DNA
448 <213> ORGANISM: Arabidopsis thaliana
450 <220> FEATURE:
452 <221> NAME/KEY: CDS
454 <222> LOCATION: 107...2260
456 <301> AUTHORS: Yoshu Yoshiba, Tomohiro Kiyasue, Takeshi Katagiri, Hiroko
457 Ueda, Tsuyoshi Mizoguchi, Kazuko Yamaguchi-Shinozaki, Keishiro
458 Wada, Yoshinori Harada, Kazuo Shinozaki
460 <302> TITLE: Correlation between the induction of a gene for 1-
461 pyrroline-5-carboxylate synthetase and the accumulation of
462 proline in Arabidopsis thaliana under osmotic stress.
464 <303> JOURNAL: The Plant Journal
466 <304> VOLUME: 7

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DATE: 01/19/2002

PATENT APPLICATION: US/10/026,767

TIME: 14:40:57

Input Set : A:\PTO.txt

Output Set: N:\CRF3\01182002\J026767.raw

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468 <305> ISSUE: 5
470 <306> PAGES: 751-760
472 <307> DATE: 1995-01-20
474 <308> DATABASE ACCESSION NO: D32138
476 <309> DATABASE ENTRY DATE: 1994-07-12
478 <400> SEQUENCE: 2
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486                                     Met Glu Glu
488                                     1
492 cta gat cgt tca cgt gct ttt gcc aga gac gtc aaa cgt atc gtc gtt 163
494 Leu Asp Arg Ser Arg Ala Phe Ala Arg Asp Val Lys Arg Ile Val Val
496      5              10              15
500 aag gtt ggg aca gca gtt gtt act gga aaa ggt gga aga ttg gct ctt 211
502 Lys Val Gly Thr Ala Val Val Thr Gly Lys Gly Gly Arg Leu Ala Leu
504  20              25              30              35
508 ggt cgt tta gga gca ctg tgt gaa cag ctt gcg gaa tta aac tcg gat 259
510 Gly Arg Leu Gly Ala Leu Cys Glu Gln Leu Ala Glu Leu Asn Ser Asp
512              40              45              50
516 gga ttt gag gtg ata ttg gtg tca tct ggt gcg gtt ggt ctt ggc agg 307
518 Gly Phe Glu Val Ile Leu Val Ser Ser Gly Ala Val Gly Leu Gly Arg
520              55              60              65
524 caa agg ctt cgt tat cga caa tta gtc aat agc agc ttt gcg gat ctt 355
526 Gln Arg Leu Arg Tyr Arg Gln Leu Val Asn Ser Ser Phe Ala Asp Leu
528      70              75              80
532 cag aag cct cag act gaa ctt gat ggg aag gct tgt gct ggt gtt gga 403
534 Gln Lys Pro Gln Thr Glu Leu Asp Gly Lys Ala Cys Ala Gly Val Gly
536      85              90              95
540 caa agc agt ctt atg gct tac tat gag act atg ttt gac cag ctt gat 451
542 Gln Ser Ser Leu Met Ala Tyr Tyr Glu Thr Met Phe Asp Gln Leu Asp
544 100              105              110              115
548 gtg acg gca gct caa ctt ctg gtg aat gac agt agt ttt aga gac aag 499
550 Val Thr Ala Ala Gln Leu Leu Val Asn Asp Ser Ser Phe Arg Asp Lys
552              120              125              130
556 gat ttc agg aag caa ctt aat gaa act gtc aag tct atg ctt gat ttg 547
558 Asp Phe Arg Lys Gln Leu Asn Glu Thr Val Lys Ser Met Leu Asp Leu
560              135              140              145
564 agg gtt att cca att ttc aat gag aat gat gct att agc acc cga aga 595
566 Arg Val Ile Pro Ile Phe Asn Glu Asn Asp Ala Ile Ser Thr Arg Arg
568      150              155              160
572 gcc cca tat cag gat tct tct ggt att ttc tgg gat aac gat agc tta 643
574 Ala Pro Tyr Gln Asp Ser Ser Gly Ile Phe Trp Asp Asn Asp Ser Leu
576      165              170              175
580 gct gct cta ctg gcg ttg gaa ctg aaa gct gat ctt ctg att ctt ctg 691
582 Ala Ala Leu Leu Ala Leu Glu Leu Lys Ala Asp Leu Leu Ile Leu Leu
584 180              185              190              195
588 agc gat gtt gaa ggt ctt tac aca ggc cct cca agt gat cct aac tca 739
590 Ser Asp Val Glu Gly Leu Tyr Thr Gly Pro Pro Ser Asp Pro Asn Ser
592              200              205              210

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## VERIFICATION SUMMARY

DATE: 01/19/2002

PATENT APPLICATION: US/10/026,767

TIME: 14:40:58

Input Set : A:\PTO.txt

Output Set: N:\CRF3\01182002\J026767.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

10/026,767

-1-

[Sequence Listing]

*delete*

**Does Not Comply  
Corrected Diskette Needed**

<110> Hitachi, LTD.